

## AMENDMENT TO THE ABSTRACT

Please replace the abstract with the following amended abstract:

Methods for identifying a macromolecule having a sequence and sequence modifications thereof from mass spectrometry data, including a method comprising: providing at least one *de novo* sequence from mass spectroscopy data of sequences of fragments of said macromolecule, calculating at least one mass-based alignment between each *de novo* sequence and sequence in a sequence database, comparing the *de novo* sequence of a fragment containing a modification site with a sequence in the database, identifying a difference by utilizing a modification catalog, calculating at least one match score for the mass-based alignment, identifying sequences in said database from mass-based alignment in response to the match score, and grouping identification of sequences from at least one *de novo* sequence into an identified macromolecule list that agrees with the mass, and storing the result on a computer readable medium.